

SUPPLEMENTAL TABLES

Table S1: AUC scores of logistic regression models (rows) for binary classification of three protein types (columns) participating in c-di-GMP signaling network. The associated P values for some of the data in this Table are shown in **Table S2**.

	Dual	DGC	PDE
<i>eigenvector</i>	0.7371324	0.4897959	0.6613636
<i>PageRank</i>	0.7738971	0.4642857	0.6704545
<i>degree</i>	0.7564338	0.4727891	0.6636364
<i>betweenness</i>	0.7389706	0.5595238	0.5772727
<i>avg nearest neighbor deg</i>	0.6783088	0.7763605	0.5409091
<i>deg + PR + avg_nn_deg</i>	0.7628676	0.7534014	0.6795455
<i>eigen + PR + btwnnss</i>	0.9246324	0.8979592	0.7431818
<i>deg + PR + btwnnss</i>	0.8400735	0.6904762	0.6750000
<i>deg + eigen + btwnnss</i>	0.8658088	0.8843537	0.7568182
<i>eigen + deg + PR + btwnnss</i>	0.9264706	0.8962585	0.7750000
<i>all five centralities</i>	0.9191176	0.9047619	0.7840909

Table S2: P-values of each network feature in the three binary classifiers of corresponding protein types for select analyses shown in **Table S1**.

	Dual	DGC	PDE
<i>eigenvector</i>	0.009702482	0.005065715	0.366506503
<i>PageRank</i>	0.006520128	0.005662699	0.586409013
<i>betweenness</i>	0.02163542	0.01310859	0.86801627

Table S3: Linear regression model with diffused gene additive log ratios^a.

	coefficient	p-value
<i>(Intercept)</i>	0.0783049	2.01e-08 (***)
<i>wild type biofilm formation</i>	1.0129670	< 2e-16 (***)
<i>betweenness</i>	0.0001193	0.388
<i>eigenvector centrality</i>	0.0750168	1.10e-08 (***)
<i>gene expression diffused</i>	0.0016159	0.521

^aIn various simple linear regression models, gene transcription data did not show any statistical significance, including the model above: *phenotype* ~ *wild type* + *betweenness* + *eigenvector centrality* + *gene data* done in a subset of 26 environments. Note: This subset of 26 environments was chosen at random, inclusion of the whole dataset introduces more noise and does not improve statistical significance of diffused gene data.